

FIG. 1

Multiple Alignment:

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SPj	SPkinaseinHSDA59H18	MEKPYAFTVHCVKRAARRHRWKWAQVTFWCPEEQCHLWLQTLREMLEKLTSPKHLLWFI
CA	CAB62977	-----PKHLLWFI
SPj	SPkinaseinHSDA59H18	NPFGGKGQGKRIYERKVAPLFTLASITTDIGNKIFYVNYVEVITEHANQAKETLYEINID
CA	CAB62977	NPFGGKGQGKRIYERKVAPLFTLASITTDIGNKIFYVNYVEVITEHANQAKETLYEINID
SPj	SPkinaseinHSDA59H18	KYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCY
CA	CAB62977	KYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPAGSTDCVCY
SPj	SPkinaseinHSDA59H18	STVGTSDAETSALHIWVGDSLAMDVSSVHHNSTLLRYSVSLGYGFYGDIIKDSEKKRWL
CA	CAB62977	STVGTSDAETSALHIWVGDSLAMDVSSVHHNSTLLRYSVSLGYGFYGDIIKDSEKKRWL
SPj	SPkinaseinHSDA59H18	GLARYDFSGLKTFLSHHCYEGTWSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLSEEQK
CA	CAB62977	GLARYDFSGLKTFLSHHCYEGTWSFLPAQHTVGSPRDRKPCRAGCFVCRQSKQQLSEEQK
SPj	SPkinaseinHSDA59H18	KALYGLEAAEDVEEWQVVC GKFLAINATNMSCACERSPRGLSPA AHLGDGSSDLILIRKC
CA	CAB62977	KALYGLEAAEDVEEWQVVC GKFLAINATNMSCACERSPRGLSPA AHLGDGSSDLILIRKC
SPj	SPkinaseinHSDA59H18	S R F N F L R F L I R H T N Q Q D F T F V E V Y R V K K F Q T S K H M E D E D S D L K E G G K R F G H I C S S
CA	CAB62977	S R F N F L R F L I R H T N Q Q D Q -----
SPj	SPkinaseinHSDA59H18	H P S C C C T V S N S S W N C D G E V L H S P A I E V R V H C Q L V R L F A R G I E E N P K P D S H S
CA	CAB62977	-----

FIG. 2

Multiple Alignment:

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S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  PKHLLVF INPFGGKGQGR IYERKVAPLFTLASITTD IIGNKFYVNYVEVITEHANQAKE

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  TLYEINI DKYDGI VCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  GSTDCVCYSTVGTSDAETSA LHI VVGDSLAMDVSSVHHNSTLLRYSVSLGYGFYGDIIK

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  DSEKKRWLGLARYDFSGLKTF LSHHCYEGTVSFLPAQHTVGSPRDRKPCRAGCFVCRQSK

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  QQLEEEQKKALYGLEAAEDVEEWQVVC GKFLA INATNMSCACRSPRG LSPA AHLGDGSS

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  DLILIRKCSRNFRLRFLIRHTNQEDQFGFTFVEVYRVVKKFTQFTSKHVEDNDNLKELEKQ
DLILIRKCSRNFRLRFLIRHTNQDQFDFTFVEVYRVVKKFTQFTSKHVEDEDSDLKEGGKK

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  KFGKICKDRPSC TCSASRSSWNCDGEV LHS PAIEVRVHCQLVRLFARGIEEES
KFGQICKDNPPCACTSSRSSWNCDGEV LHS PAIEVRVHCQLVRLFARGIEEES
RFGHICSHPSCCCTVSNSSWNCDGEV LHS PAIEVRVHCQLVRLFARGIEENPKPD SHS

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FIG. 3

SPkinasemHSDA59H18	-----MEKPY-----AFTVHCVKRAKRRWVKWAQVT	
corrected_human_sphingosine	-----MDPAGGPRGVLP-PC-F	C1
AF068748_EXT-2	-----MSPYECPRGLLP-PC-F	
Q06147	LYIDYKPHSS-SHLKEE-DDLVEFELKRSYKNTRENE-S	
Q12246	LLIDHVSRSKRANTGEENISSGTVEELKKSSENSENE-S	
Q14159	CWVDFVENS-----QFCEYLQVATKGIKSE-F	
Q18425	CRSDAEENEQ-----LTSVLSRKPPPEQCQGN	
SPkinasemHSDA59H18	FWCPEEQECH-----LWLQTLREMLEKLTSPK-F	
corrected_human_sphingosine	SHWQFLAEAEISFTIMLTER-----RNHARELVE--S	C2
AF068748_EXT-2	SKQPFLEEAEISFKLYTER-----KNHARELVC--A	
Q06147	TKAKFLLASRCISIVYTYKY-----PGHAIETAK--E	
Q12246	TKAKFLVESGCKIEAVTYKY-----ARHAIETAK--D	
Q14159	SEADPFSSAHSSICEVYTER-----KDHAETAK--N	
Q18425	NTGPKDKSLIRYDVVITG-----PNHAENYLMT--K	
SPkinasemHSDA59H18	RKHAFCTLASIFETBYGNLFYVNVYEVITEHANQAKETLYE	
corrected_human_sphingosine	HEVHGLMERPD--WETAIQKPECSEAGSGNAASINH	C3
AF068748_EXT-2	HEVHGLMERPD--WETAIQKPECSEAGSGNAASVNH	
Q06147	HEVHGLYQRPD--VKAFNNIAETPCGSGNAMSYS-CH	
Q12246	YEYHGLYRPD--VDAFNKLAATQPCGSGNAMSIS-CH	
Q14159	HEVHGLGERD--LEAFKLPFCMSEAGSGNAFSYN--A	
Q18425	FEALHGHCREDA--ERIFPTPLGISESGNGLLCSVLS	
SPkinasemHSDA59H18	SEVHGLFEGRTQSAGVDQNHPRAVLWESSLRIGTIPAGSTD	
corrected_human_sphingosine	LCRPVLSPMNLLSLHTASGLRS--SVLSAAGFIADT	C4
AF068748_EXT-2	LCRRRISPMNLLSLHTASGLRL--SVLSAAGFIADT	
Q06147	SIEIRIDLMCCSQPSYAREHPKISFLSQTGCIATDIN	
Q12246	SIEIRIDLMCCSQPSYMNWPRISFLSQTGCIATDIN	
Q14159	GRPISFDLMTFEQ--KGKKAISFLRANYGFIADCDIG	
Q18425	TSPHAKAESVALYSVKTDNQSYAFLSGMGEMADIDSE	
SPkinasemHSDA59H18	I VVGDSLAMDVSSVHHNSTLLRYSVSLGFGFYGLIK	
corrected_human_sphingosine	AALSTYRRLATLEVGTVGF-----ETP-----	
AF068748_EXT-2	ASLBITYOQLAYLEVGTVAS-----ETP-----	
Q06147	IQKKKYPCEIYVKYAAKSKNELKNHYLEH--NGS	
Q12246	IQKKKYPCEYFVKYAAKSKKELKVHFLNEDH--	
Q14159	FQKPDWKCISEMDVVS SDRTETKHMVE--LSK--	
Q18425	CRLBSYKERTTYRKYKPKGFHPSSNVFSVYEK--	
SPkinasemHSDA59H18	L SHHCYESTYSFLRAQHTVGSPPED-----KKP--	
corrected_human_sphingosine	-----ASPVSVQQ-----GPWDAHLVPLEEQ--	
AF068748_EXT-2	-----ASTLVQK-----GPWDTHLVPLEEP--	
Q06147	ENEDEDADADDEDSHLISRDLEADSSADQ--KEED	
Q12246	SPDLLSKNNINNSTKDEESPNFLN-----EDNFK	
Q14159	-----N-----LAPMSES-----SDSKTVST	
Q18425	-DSKVKTNGSVSDSEETMETKFQN-----WTL	
SPkinasemHSDA59H18	QSKQLEEEQKKALYGLEAAEDVEEWQVVGCKFLA	
corrected_human_sphingosine	EDFVLVLALLHSHLSKMFAPMGRCAASVHHLFY	
AF068748_EXT-2	QDFVLVLVLLHTLSSELFAAPMGRCEASVHHLFY	
Q06147	NNLGIFYTGMKPYAAATKFFPALPDSGTMDMVETD	
Q12246	DNLITFYTGKMPYAAATKFFPALPADGTEDLVETD	
Q14159	NDLISFCAGLEPYAAPDAKMFPASNDNGLIDVAVY	
Q18425	DNFVNKYAVTLRHIAADGPFAPASAKLEDNRHLSY	
SPkinasemHSDA59H18	GSSDLELIRKCKRFNFLRLIRHTNQDQDFTFE	
corrected_human_sphingosine	ECVLYYYPVYAKKLEPKDCKG--VFANDGE	C5
AF068748_EXT-2	DCVLYYYPVYAKKLEPKSQRG--VFSVDGE	
Q06147	LQPEVLSKIIAKKIPKLGNG--LFSVDGEKFP	
Q12246	LEPEVLSKIIAKKIPKYESG--LFSVDGEKFP	
Q14159	YSKHLNYYKVRSEKFTP--VNTGKRYVFANDGES	
Q18425	DLFVKHVEVSSMKEEVIS EGS--HVVLEDGEY	
SPkinasemHSDA59H18	GKKRFGHLCSSHPSCCCTQSNS--SWNCDGE	
corrected_human_sphingosine	WKPOQMPPPEEPL	
AF068748_EXT-2	RDSRRGPPPEEP-	
Q06147	-NGRYDIDTFDSM	
Q12246	-NGRYDIDTFDSM	
Q14159	AGQLLDI-----	
Q18425	-----	
SPkinasemHSDA59H18	-GIEENPKPDSSH	

FIG. 4

PHYLIP - Protein Distance Analysis

Sequences analyzed:

- 1. SPkinaseinHSDA59H18
- 2. Q18425
- 3. O14159
- 4. Q06147
- 5. Q12246
- 6. coorrected\_human\_sphingosine
- 7. AF068748\_EXT-2

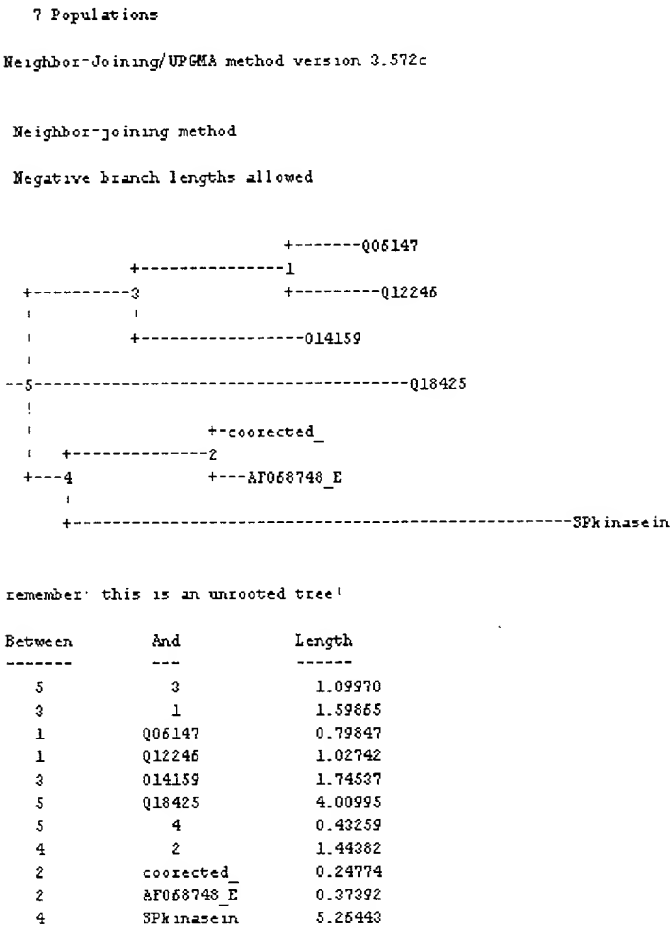


FIG. 5

Multiple Alignment:

80432911	SPkinaseinHSDA59H18	AGAPGADACSVPS E I I AVEETDVHGKHQSGKWQKMEKPYAFTVHCVKRA ERHRWKWAQ -----MEKPYAFTVHCVKRA ERHRWKWAQ
80432911	SPkinaseinHSDA59H18	WTFWCPEEQCHLWLQTLREMLEKLTSPKHL V F INPFGKGQGGKRIYE RKVAPLFTLA WTFWCPEEQCHLWLQTLREMLEKLTSPKHL V F INPFGKGQGGKRIYE RKVAPLFTLA
80432911	SPkinaseinHSDA59H18	SITTDI I -----YTEHANQAKETLYEIN IDKYDGI VCVGGDGMFSEVLHGL I GR SITTDI I GNKFFYN YVEWTEHANQAKETLYEIN IDKYDGI VCVGGDGMFSEVLHGL I GR
80432911	SPkinaseinHSDA59H18	TQRSAGVDQNHPR ----- TQRSAGVDQNHPR A VLPSSLRIGI IPAGSTDC V CYSTWGTSDAETSA LHI VWGDSLAMD
80432911	SPkinaseinHSDA59H18	WSSVHHNSTLLRYS V SLLGYGFYGD I IKDSEKKRWLGLARYDFSGLKTFL SHHCYEGT VS -----
80432911	SPkinaseinHSDA59H18	FLPAQHTVGSPEDRKPCRAGCFVCRQSKQQL EEE QKKALYGLEAAEDVEEWQVVC GKFLA -----
80432911	SPkinaseinHSDA59H18	INATNMSCACRRS P RGLSPA AHLGDSSDL I I R KCSRFNFLRFLIRHTNQDQDFDFT FY -----
80432911	SPkinaseinHSDA59H18	EYVRVKKFQFTSKHMEDEDS DLKEGKKRFGHI C S SHPSCCCTVSNSSWNCDGEVLHSPA -----
80432911	SPkinaseinHSDA59H18	IEVRVHCQLVELFA RGI EENPKPSHS -----